

AMENDMENTS TO THE CLAIMS

Please amend 1, 3, 5, 6, 9, 11-19, 21-26, 28, 31, 33-39 and 43-52 as shown in the following listing of the claims:

1. (Currently Amended) Isolated polynucleotides coding for a ferroportin1 mutated in one of the following amino acids:
 - amino acid at position 80 of seq ~~IDN2~~ SEQ ID NO:2,
 - amino acid at position 174 of seq ~~IDN2~~ SEQ ID NO:2,
 - amino acid at position 248 of seq ~~IDN2~~ SEQ ID NO:2, as compared to the wild type sequence.
2. (Original) Polynucleotide according to claim 1 characterized in that the amino acid at position 80 is different from Glycine.
3. (Currently Amended) Polynucleotide according to claim 2 characterized by having a polymorphism at nucleotide 238 of ~~IDN1-sequence~~ SEQ ID NO:1.
4. (Original) Polynucleotide according to claim 3 characterized in that said polymorphism is a substitution of a G with an A.
5. (Currently Amended) ~~Polinucleotide~~ polynucleotide according to claim 1 ~~characterized~~ characterized in that said amino acid at position 174 is different from Asparagine.
6. (Currently Amended) ~~Polinucleotide~~ polynucleotide according to claim 5 characterized by having a polymorphism at nucleotide 521 of ~~IDN1-sequence~~ SEQ ID NO:1.
7. (Original) Polynucleotide according to claim 6 characterized in that said polymorphism is a substitution of an A with a T.
8. (Original) Polynucleotide according to claim 1 characterized in that the amino acid at position 248 is different from Glutamine.

9. (Currently Amended) Polynucleotide according to claim 8 characterized by having a polymorphism at nucleotide 744 of ~~IDN1-sequence~~ SEQ ID NO:1.
10. (Original) Polynucleotide according to claim 9 characterized in that said polymorphism is a substitution of a G with a T.
11. (Currently Amended) Polynucleotide according to ~~anyone of claims 1-10~~ claim 1 characterized in that it is genomic DNA.
12. (Currently Amended) Polynucleotide according to ~~anyone of claims 1-10~~ claim 1 characterized in that it is mRNA.
13. (Currently Amended) Polynucleotide according to ~~anyone of claims 1-10~~ claim 1 characterized in that it is cDNA.
14. (Currently Amended) Polynucleotide coding for a mutated ferroportin 1 according to claim 1 characterized in that its nucleotide sequence corresponds to ~~seqIDN3 or to seqIDN5 or to seqIDN7~~ SEQ ID NO:3, 5, or 7.
15. (Currently Amended) Polynucleotide carrying at least 10 consecutive nucleotides derived from ~~anyone~~ any one of sequences ~~seqIDN3 or to seqIDN5 or to seqIDN7~~ SEQ ID NO:3, 5, or 7, and characterized by comprising at least one of polymorphic nucleotides respectively selected from the group consisting of :
- polymorphism corresponding to position 238 of ~~seqIDN3~~ SEQ ID NO:3,
 - ~~polymorphism~~ polymorphism corresponding to position 521 of ~~seqIDN5~~ SEQ ID NO:5, or
 - polymorphism corresponding to position 744 of ~~seqIDN7~~ SEQ ID NO:7.
16. (Currently Amended) Polynucleotide according to claim 15 characterized by comprising at least one of the oligonucleotides corresponding to sequences ~~IDN9-27~~ SEQ ID NO: 9-27.

17. (Currently Amended) Polynucleotide having a complementary sequence as compared to ~~anyone of the polynucleotide according to elaims 14-16~~ claim 15.
18. (Currently Amended) Polynucleotide according to ~~elaims 1-16~~ claim 1 characterized in that it is labelled.
19. (Currently Amended) Recombinant vector characterized by comprising the polynucleotide according to ~~elaims 1-17~~ claim 1.
20. (Original) Isolated cell characterized in that it is transfected or transformed with the recombinant vector according to claim 19.
21. (Currently Amended) Eukaryotic cell, tissue or non-human animal including a transgene where such transgene is at least a polynucleotide according to ~~elaims 1-16~~ claim 1.
22. (Currently Amended) Mutated ferroportin1 coded by anyone of the polynucleotide according to ~~elaims 1-16~~ claim 1.
23. (Currently Amended) Mutated ferroportin1 according to claim 22 having amino acid sequence corresponding to ~~anyone~~ any one of sequence ~~IDN 4,6, 8~~ SEQ ID NO: 4, 6, or 8 or fragments thereof.
24. (Currently Amended) Peptide comprising at least 6 consecutive amino acids derived from at least one of the sequences selected from the group consisting of : ~~seq IDN 4,6, 8~~ SEQ ID NO: 4, 6, or 8 and characterized by comprising at least one of the mutated amino acids at position corresponding to positions 80,174, 248 of ~~seq IDN2~~ SEQ ID NO:2.
25. (Currently Amended) Polynucleotides according to ~~elaims 1-17~~ claim 1 for therapeutic use.
26. (Currently Amended) Peptides ~~according~~ according to claim 24 for therapeutic use.
27. (Original) Mutated ferroportin 1 according to claim 23 for therapeutic use.

28. (Currently Amended) Method to detect polymorphisms in the ferroportin gene in vitro characterized by using at least one of the polynucleotides according to ~~claims 1-18~~ claim 1.

29. (Original) Method according to claim 28 wherein said polymorphisms are associated to hyperferritinemia or anemia.

30. (Original) Method according to claim 28 for the in vitro diagnosis of non-HFE Hereditary Hemochromatosis in a mammal including the following steps:

a) isolation of genomic DNA or RNA by a biological sample obtained from a mammal.

b) evaluation of the presence in said genomic DNA or RNA of at least one of the polymorphisms according to claim 4, 7 or 10, wherein the presence of said polymorphisms is an indication that said mammal is affected by non-HFE Hereditary Hemochromatosis or is prone to develop said disease

31. (Currently Amended) Method according to claim 28 for the in vitro diagnosis of an impaired iron homeostasis consisting essentially in the evaluation of the presence in a sample of genomic DNA, RNA or cDNA of at least one of the polymorphisms selected from the group consisting of: polymorphism corresponding to position 238 of ~~seqIDN3~~ SEQ ID NO:3, polymorphism corresponding to position 521 of ~~seqIDN5~~ SEQ ID NO:5 or polymorphism corresponding to position 744 of ~~seqIDN7~~ SEQ ID NO:7.

32. (Original) Method according to claim 31 where such iron impaired homeostasis is anemia or hyperferritinemia, African or Bantu siderosis, or non-HFE Hereditary Hemochromatosis.

33. (Currently Amended) Method according to claim 32 for the in vitro diagnosis of African Siderosis or Bantu Hemochromatosis in a mammal including the following steps:

a) Isolation of genomic DNA or RNA from a biological sample obtained by said mammal.

b) evaluation of the presence in said genomic DNA or RNA of a polymorphism in the nucleotide corresponding to nucleotide 744 of ~~seq ID NO:1~~ SEQ ID NO:1 wherein the presence of such polymorphism is an indication that said mammal is affected by African Siderosis, Bantu Haemochromatosis or is prone to develop said disease.

34. (Currently Amended) Method according to the ~~claims 30-33~~ claim 30 characterized in that before said evaluation the RNA is transcribed into cDNA by reverse transcriptase.

35. (Currently Amended) Method according to the ~~claims 30-33~~ claim 30 wherein the evaluation is performed after the amplification by PCR with a suitable oligonucleotide pair, of a DNA fragment comprising at least one of the following polymorphic nucleotides : nucleotide corresponding to position 238, nucleotide corresponding to position 521, nucleotide corresponding to position 744 of ~~seq ID NO:1~~ SEQ ID NO:1.

36. (Currently Amended) Method according to claim 35 characterized in that in said amplification at least one of the following oligonucleotides : ~~IDN 13,14, 19, 20~~ SEQ ID NO:13,14, 19, or 20 are used.

37. (Currently Amended) Method according to ~~claims 30-36~~ claim 30 characterized in that said mammal is Homo Sapiens.

38. (Currently Amended) Method according to ~~claims 30-36~~ claim 30 characterized in that said biological sample is a sample of blood, plasma, saliva, urina, faeces, amniotic liquid or tissue.

39. (Currently Amended) Method according to the ~~claims 30-36~~ claim 30 characterized in that said evaluation is performed by a technique selected from the group consisting of: gain or loss of a cleavage site for a restriction enzyme, hybridization techniques with allele-specific oligonucleotide probes ~~according to the claims 15-17~~, allele specific PCR, mismatch repair detection, single strand conformational polymorphism analysis, gel electrophoresis on denaturing gradient, hot cleavage, DNase and RNase protection assay, allele specific primer

~~extension~~ extension, genetic bit analysis oligonucleotide-ligation assay, allele specific ligation chain reaction and sequencing techniques.

40. (Original) Method according to claim 39 characterized in that said evaluation is performed by techniques based on the use of restriction enzymes, allele specific PCR, hybridization techniques, or sequencing techniques.

41. (Original) Method according to claim 40 wherein said restriction enzymes are chosen among the following : TspR1, Bsml, Pvull.

42. (Original) Method for the in vitro diagnosis of Hereditary Hemochromatosis in a mammal comprising the evaluation of the presence in a biological sample obtained by said mammal of a mutated ferroportin 1 protein according to claim 22, wherein the presence of said protein is an indication that said mammal is affected by Hereditary Hemochromatosis.

43. (Currently Amended) Method according to claim 42 ~~wherein~~ wherein said identification is performed by using antibodies able to specifically detect said mutated ferroportin 1 protein.

44. (Currently Amended) Monoclonal or polyclonal antibody able to specifically detect a mutated ferroportin1 protein according to ~~claims 22-23~~ claim 22.

45. (Currently Amended) Use of ~~antibodies according to claim 44~~ a monoclonal or polyclonal antibody able to specifically detect a mutated ferroportin1 protein according to claim 22 for the specific inactivation of ~~a mutated ferroportin 1 protein according to claim 22~~ said mutated ferroportin 1 protein.

46. (Currently Amended) "Computer readable" support characterized by comprising at least one of the polynucleotides according to ~~claims 1-17~~ claim 1.

47. (Currently Amended) Use of ~~polinucleotides~~ polynucleotides according to ~~claims 1-17~~ claim 1 for the detection of polymorphisms in the ferroportin gene.

48. (Currently Amended) Use of polynucleotides according to ~~claims 1-17~~ claim 1 for the preparation of a pharmaceutical composition for the treatment of impaired iron homeostasis disease.
49. (Currently Amended) Use of polynucleotides according to ~~claims 1-17~~ claim 1 to modulate the expression of the gene coding for a mutated ferroportin1.
50. (Currently Amended) Kit for the non-HFE hereditary Hemochromatosis diagnosis comprising at least one of the oligonucleotides according to ~~claims 1-17~~ claim 1.
51. (Currently Amended) Kit for hereditary impaired iron homeostasis diagnosis comprising at least one of the polynucleotides according to ~~claims 1-17~~ claim 1.
52. (Currently Amended) Kit for detecting a polymorphism selected from the group consisting of : polymorphism of nucleotide corresponding to position 238 of ~~seq-IDN1~~ SEQ ID NO:1, polymorphism of the nucleotide corresponding to position 521 of ~~seq-IDN1~~ SEQ ID NO:1, polymorphism of the nucleotide corresponding to position 744 of ~~sequence-IDN1~~ SEQ ID NO:1 characterized by comprising at least one of the ~~oligonucleotides~~ oligonucleotides of sequence: ~~IDN13, IDN14, IDN19, IDN20~~ SEQ ID NO: 13, 14, 19 or 20 optionally in combination with at least one of the following restriction enzymes: TspR1, BsmI, PvuII.